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Projects

Former Projects

Integration of transcriptome and proteome data from human-pathogenic fungi

[Details](#)

Automated analysis of dynamic properties in biological systems from image data

[Details](#)

Prediction of gene regulatory networks involved in the differentiation, secondary metabolism and cross talk of *Aspergillus nidulans*

[Details](#)

Bioinformatic investigation and prediction of gene regulatory elements in pathogenic fungi

[Details](#)

Optimization of the influenza neuraminidase inhibitor therapy by use of secondary bacterial infections

[Details](#)

Integrated genome-wide data analysis by ensemble learning methods to understand infection processes

[Details](#)

Analysis and interpretation of variance in gene expression data

[Details](#)